

Guangfu Jin

List of Publications by Year in descending order

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Version: 2024-02-01

178
papers

7,133
citations

87888

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h-index

74163

75
g-index

184
all docs

184
docs citations

184
times ranked

12749
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic risk, metabolic syndrome, and gastrointestinal cancer risk: A prospective cohort study. Cancer Medicine, 2023, 12, 597-605.	2.8	6
2	Identification of A-to-I RNA editing profiles and their clinical relevance in lung adenocarcinoma. Science China Life Sciences, 2022, 65, 19-32.	4.9	6
3	Circulating C-reactive protein increases lung cancer risk: Results from a prospective cohort of <sc>UK</sc> Biobank. International Journal of Cancer, 2022, 150, 47-55.	5.1	15
4	Adherence to Healthy Lifestyle and Liver cancer in Chinese: a prospective cohort study of 0.5 million people. British Journal of Cancer, 2022, 126, 815-821.	6.4	15
5	Prevalence of <sc><i>Helicobacter pylori</i></sc> infection in China: A systematic review and meta-analysis. Journal of Gastroenterology and Hepatology (Australia), 2022, 37, 464-470.	2.8	94
6	Hypomethylation-activated cancer-testis gene LIN28B promotes cell proliferation and metastasis in gastric cancer. Gene, 2022, 813, 146115.	2.2	6
7	Association of Maternal Dietary Patterns during Gestation and Offspring Neurodevelopment. Nutrients, 2022, 14, 730.	4.1	12
8	Association Between Neuroticism and Risk of Lung Cancer: Results From Observational and Mendelian Randomization Analyses. Frontiers in Oncology, 2022, 12, 836159.	2.8	1
9	Association between <i>Helicobacter pylori</i> antibodies determined by multiplex serology and gastric cancer risk: A meta-analysis. Helicobacter, 2022, 27, e12881.	3.5	13
10	A polygenic risk score for nasopharyngeal carcinoma shows potential for risk stratification and personalized screening. Nature Communications, 2022, 13, 1966.	12.8	19
11	Comprehensive functional annotation of susceptibility variants identifies genetic heterogeneity between lung adenocarcinoma and squamous cell carcinoma. Frontiers of Medicine, 2021, 15, 275-291.	3.4	21
12	Pre-diagnostic circulating concentrations of insulin-like growth factor-1 and risk of COVID-19 mortality: results from UK Biobank. European Journal of Epidemiology, 2021, 36, 311-318.	5.7	19
13	A nomogram for predicting lymph node metastasis in superficial esophageal squamous cell carcinoma. Journal of Biomedical Research, 2021, 35, 361.	1.6	1
14	Prediction of live birth probability after in vitro fertilization and intracytoplasmic sperm injection treatment: A multi-center retrospective study in Chinese population. Journal of Obstetrics and Gynaecology Research, 2021, 47, 1126-1133.	1.3	5
15	Assisted reproductive technology and birth defects in a Chinese birth cohort study. The Lancet Regional Health - Western Pacific, 2021, 7, 100090.	2.9	24
16	Prediction and clinical utility of a liver cancer risk model in Chinese adults: A prospective cohort study of 0.5 million people. International Journal of Cancer, 2021, 148, 2924-2934.	5.1	6
17	Genetic variants associated with expression of TCF19 contribute to the risk of head and neck cancer in Chinese population. Journal of Medical Genetics, 2021, , jmedgenet-2020-107410.	3.2	7
18	Relationships between sleep traits and lung cancer risk: a prospective cohort study in UK Biobank. Sleep, 2021, 44, .	1.1	26

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19	A cross-tissue transcriptome-wide association study identifies novel susceptibility genes for lung cancer in Chinese populations. <i>Human Molecular Genetics</i> , 2021, 30, 1666-1676.	2.9	9
20	Potential functional variants of KIAA genes are associated with breast cancer risk in a case control study. <i>Annals of Translational Medicine</i> , 2021, 9, 549-549.	1.7	1
21	Sex-specific associations of circulating testosterone levels with all-cause and cause-specific mortality. <i>European Journal of Endocrinology</i> , 2021, 184, 723-732.	3.7	17
22	Association of assisted reproductive technology, germline de novo mutations and congenital heart defects in a prospective birth cohort study. <i>Cell Research</i> , 2021, 31, 919-928.	12.0	26
23	Genome-wide gene-smoking interaction study identified novel susceptibility loci for non-small cell lung cancer in Chinese populations. <i>Carcinogenesis</i> , 2021, 42, 1154-1161.	2.8	1
24	Genetic Risk for Overall Cancer and the Benefit of Adherence to a Healthy Lifestyle. <i>Cancer Research</i> , 2021, 81, 4618-4627.	0.9	48
25	Whole-exome sequencing reveals common and rare variants in immunologic and neurological genes implicated in achalasia. <i>American Journal of Human Genetics</i> , 2021, 108, 1478-1487.	6.2	6
26	Diet and Risk of Incident Lung Cancer: A Large Prospective Cohort Study in UK Biobank. <i>American Journal of Clinical Nutrition</i> , 2021, 114, 2043-2051.	4.7	38
27	LncPSCA in the 8q24.3 risk locus drives gastric cancer through destabilizing DDX5. <i>EMBO Reports</i> , 2021, 22, e52707.	4.5	18
28	The rates and medical necessity of cesarean delivery in China, 2012-2019: an inspiration from Jiangsu. <i>BMC Medicine</i> , 2021, 19, 14.	5.5	8
29	Stress, anxiety, and depression in infertile couples are not associated with a first IVF or ICSI treatment outcome. <i>BMC Pregnancy and Childbirth</i> , 2021, 21, 725.	2.4	6
30	Tea consumption and risk of stroke in Chinese adults: a prospective cohort study of 0.5 million men and women. <i>American Journal of Clinical Nutrition</i> , 2020, 111, 197-206.	4.7	27
31	Cancer incidence in relation to body fatness among 0.5 million men and women: Findings from the China Kadoorie Biobank. <i>International Journal of Cancer</i> , 2020, 146, 987-998.	5.1	19
32	Meta-analysis of genome-wide association studies and functional assays decipher susceptibility genes for gastric cancer in Chinese populations. <i>Gut</i> , 2020, 69, 641-651.	12.1	36
33	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. <i>Genomics</i> , 2020, 112, 1223-1232.	2.9	15
34	Genetic risk, incident gastric cancer, and healthy lifestyle: a meta-analysis of genome-wide association studies and prospective cohort study. <i>Lancet Oncology</i> , The, 2020, 21, 1378-1386.	10.7	123
35	Comprehensive characterization of functional eRNAs in lung adenocarcinoma reveals novel regulators and a prognosis-related molecular subtype. <i>Theranostics</i> , 2020, 10, 11264-11277.	10.0	20
36	In vitro activity of new tetracycline analogues omadacycline and eravacycline against clinical isolates of <i>Helicobacter pylori</i> collected in China. <i>Diagnostic Microbiology and Infectious Disease</i> , 2020, 98, 115129.	1.8	4

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37	Analysis of the interaction effect of 48 SNPs and obesity on type 2 diabetes in Chinese Hans. <i>BMJ Open Diabetes Research and Care</i> , 2020, 8, e001638.	2.8	4
38	Integration of GWAS and eQTL Analysis to Identify Risk Loci and Susceptibility Genes for Gastric Cancer. <i>Frontiers in Genetics</i> , 2020, 11, 679.	2.3	10
39	Alterations of gut microbiota composition in neonates conceived by assisted reproductive technology and its relation to infant growth. <i>Gut Microbes</i> , 2020, 12, 1794466.	9.8	9
40	Identification of Recurrent Variants in BRCA1 and BRCA2 across Multiple Cancers in the Chinese Population. <i>BioMed Research International</i> , 2020, 2020, 1-11.	1.9	4
41	Effect of endometrial thickness and embryo quality on live-birth rate of fresh IVF/ICSI cycles: a retrospective cohort study. <i>Reproductive Biology and Endocrinology</i> , 2020, 18, 89.	3.3	18
42	Remote modulation of lncRNA <i>Gclet</i> by risk variant at 16p13 underlying genetic susceptibility to gastric cancer. <i>Science Advances</i> , 2020, 6, eaay5525.	10.3	23
43	Functional genetic variants in centrosome-related genes CEP72 and YWHAG confer susceptibility to gastric cancer. <i>Archives of Toxicology</i> , 2020, 94, 2861-2872.	4.2	13
44	A nomogram for prediction of stage III/IV gastric cancer outcome after surgery: A multicenter population-based study. <i>Cancer Medicine</i> , 2020, 9, 5490-5499.	2.8	13
45	Transcriptome-wide association study for persistent hepatitis B virus infection and related hepatocellular carcinoma. <i>Liver International</i> , 2020, 40, 2117-2127.	3.9	6
46	Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China. <i>Science China Life Sciences</i> , 2020, 63, 706-711.	4.9	1,090
47	Family-based whole-genome sequencing identifies compound heterozygous protein-coding and noncoding mutations in tetralogy of Fallot. <i>Gene</i> , 2020, 741, 144555.	2.2	8
48	Vitamin D Status and Risk of All-Cause and Cause-Specific Mortality in a Large Cohort: Results From the UK Biobank. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e3606-e3619.	3.6	60
49	Genetic Association of Plasma Homocysteine Levels with Gastric Cancer Risk: A Two-Sample Mendelian Randomization Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 487-492.	2.5	4
50	Systematic analyses of genetic variants in chromatin interaction regions identified four novel lung cancer susceptibility loci. <i>Journal of Cancer</i> , 2020, 11, 1075-1081.	2.5	16
51	Genetic Variations in miR-30 Family Member Regulatory Regions Are Associated with Breast Cancer Risk in a Chinese Population. <i>BioMed Research International</i> , 2020, 2020, 1-8.	1.9	1
52	Association Analysis of Driver Gene-Related Genetic Variants Identified Novel Lung Cancer Susceptibility Loci with 20,871 Lung Cancer Cases and 15,971 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1423-1429.	2.5	6
53	Multi-marker analysis of genomic annotation on gastric cancer GWAS data from Chinese populations. <i>Gastric Cancer</i> , 2019, 22, 60-68.	5.3	8
54	Identification of risk loci and a polygenic risk score for lung cancer: a large-scale prospective cohort study in Chinese populations. <i>Lancet Respiratory Medicine</i> , 2019, 7, 881-891.	10.7	167

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55	Fine Mapping in Chromosome 3q28 Identified Two Variants Associated with Lung Cancer Risk in Asian Population. <i>Journal of Cancer</i> , 2019, 10, 1862-1869.	2.5	1
56	Mendelian randomization study of telomere length and lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2019, 8, 7469-7476.	2.8	15
57	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. <i>Carcinogenesis</i> , 2019, 40, 263-268.	2.8	3
58	The inherited variations of a p53-responsive enhancer in 13q12.12 confer lung cancer risk by attenuating TNFRSF19 expression. <i>Genome Biology</i> , 2019, 20, 103.	8.8	27
59	Telomere length in cervical exfoliated cells, interaction with HPV genotype, and cervical cancer occurrence among high-risk HPV-positive women. <i>Cancer Medicine</i> , 2019, 8, 4845-4851.	2.8	6
60	Identification of Novel T1D Risk Loci and Their Association With Age and Islet Function at Diagnosis in Autoantibody-Positive T1D Individuals: Based on a Two-Stage Genome-Wide Association Study. <i>Diabetes Care</i> , 2019, 42, 1414-1421.	8.6	60
61	Leukocyte telomere length, lipid parameters and gestational diabetes risk: a case-control study in a Chinese population. <i>Scientific Reports</i> , 2019, 9, 8483.	3.3	10
62	Associations Between Hepatitis B Virus Infection and Risk of All Cancer Types. <i>JAMA Network Open</i> , 2019, 2, e195718.	5.9	114
63	Comprehensive characterization of cancer-testis genes in testicular germ cell tumor. <i>Cancer Medicine</i> , 2019, 8, 3511-3519.	2.8	22
64	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <i>Molecular Carcinogenesis</i> , 2019, 58, 1303-1313.	2.7	6
65	A genetic variation in the CpG island of pseudogene <i>GBAP1</i> promoter is associated with gastric cancer susceptibility. <i>Cancer</i> , 2019, 125, 2465-2473.	4.1	25
66	Blood groups A and AB are associated with increased gastric cancer risk: evidence from a large genetic study and systematic review. <i>BMC Cancer</i> , 2019, 19, 164.	2.6	30
67	A nomogram to predict overall survival of patients with early stage non-small cell lung cancer. <i>Journal of Thoracic Disease</i> , 2019, 11, 5407-5416.	1.4	16
68	A clinical, biologic and mechanistic analysis of the role of ZNF692 in cervical cancer. <i>Gynecologic Oncology</i> , 2019, 152, 396-407.	1.4	10
69	Association of Mosaic Loss of Chromosome Y with Lung Cancer Risk and Prognosis in a Chinese Population. <i>Journal of Thoracic Oncology</i> , 2019, 14, 37-44.	1.1	19
70	A cancer-testis non-coding RNA LIN28B-AS1 activates driver gene LIN28B by interacting with IGF2BP1 in lung adenocarcinoma. <i>Oncogene</i> , 2019, 38, 1611-1624.	5.9	61
71	Fine mapping the MHC region identified rs4997052 as a new variant associated with nonobstructive azoospermia in Han Chinese males. <i>Fertility and Sterility</i> , 2019, 111, 61-68.	1.0	7
72	Cross-Cancer Pleiotropic Analysis Reveals Novel Susceptibility Loci for Lung Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 1492.	2.8	6

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73	Interaction analysis between germline susceptibility loci and somatic alterations in lung cancer. <i>International Journal of Cancer</i> , 2018, 143, 878-885.	5.1	13
74	Association of 48 type 2 diabetes susceptibility loci with fasting plasma glucose and lipid levels in Chinese Hans. <i>Diabetes Research and Clinical Practice</i> , 2018, 139, 114-121.	2.8	4
75	Mitochondrial DNA copy number is associated with risk of head and neck squamous cell carcinoma in Chinese population. <i>Cancer Medicine</i> , 2018, 7, 2776-2782.	2.8	15
76	<i>ATG12</i> expression quantitative trait loci associated with head and neck squamous cell carcinoma risk in a Chinese Han population. <i>Molecular Carcinogenesis</i> , 2018, 57, 1030-1037.	2.7	13
77	An esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of <i>BARX1</i> . <i>Cancer Letters</i> , 2018, 421, 103-111.	7.2	13
78	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. <i>Gene</i> , 2018, 651, 1-8.	2.2	15
79	A nomogram to predict the survival of stage IIIA-N2 non-small cell lung cancer after surgery. <i>Journal of Thoracic and Cardiovascular Surgery</i> , 2018, 155, 1784-1792.e3.	0.8	45
80	The functional polymorphisms of <i>ARID5B</i> and <i>IKZF1</i> are associated with acute myeloid leukemia risk in a Han Chinese population. <i>Gene</i> , 2018, 647, 115-120.	2.2	4
81	A novel plasma circular <i>scRNA</i> <i>circFARSA</i> is a potential biomarker for non-small cell lung cancer. <i>Cancer Medicine</i> , 2018, 7, 2783-2791.	2.8	167
82	Genome-wide association studies identified loci contribute to phenotypic variance of gastric cancer. <i>Gut</i> , 2018, 67, 1366-1368.	12.1	3
83	Integrating expression-related SNPs into genome-wide gene and pathway-based analyses identified novel lung cancer susceptibility genes. <i>International Journal of Cancer</i> , 2018, 142, 1602-1610.	5.1	14
84	Gastric cancer may share genetic predisposition with esophageal squamous cell carcinoma in Chinese populations. <i>Journal of Human Genetics</i> , 2018, 63, 1159-1168.	2.3	5
85	Genetic variants in nuclear DNA along with environmental factors modify mitochondrial DNA copy number: a population-based exome-wide association study. <i>BMC Genomics</i> , 2018, 19, 752.	2.8	16
86	Fine mapping in <i>TERT</i> - <i>CLPTM1L</i> region identified three independent lung cancer susceptibility signals: A large-scale multi-ethnic population study. <i>Molecular Carcinogenesis</i> , 2018, 57, 1289-1299.	2.7	5
87	Whole-genome sequencing reveals genomic signatures associated with the inflammatory microenvironments in Chinese NSCLC patients. <i>Nature Communications</i> , 2018, 9, 2054.	12.8	68
88	Genetically determined height was associated with lung cancer risk in East Asian population. <i>Cancer Medicine</i> , 2018, 7, 3445-3452.	2.8	6
89	Genetic variants within 17q12 are associated with the risk of cervical cancer in the Han Chinese population. <i>Gene</i> , 2018, 678, 124-128.	2.2	3
90	Influencing factors of pregnancy loss and survival probability of clinical pregnancies conceived through assisted reproductive technology. <i>Reproductive Biology and Endocrinology</i> , 2018, 16, 74.	3.3	33

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91	Germline genetic variants were interactively associated with somatic alterations in gastric cancer. <i>Cancer Medicine</i> , 2018, 7, 3912-3920.	2.8	19
92	Identification of new susceptibility loci for gastric non-cardia adenocarcinoma: pooled results from two Chinese genome-wide association studies. <i>Gut</i> , 2017, 66, 581-587.	12.1	68
93	Exome-Wide Association Study Identified New Risk Loci for Hirschsprung's Disease. <i>Molecular Neurobiology</i> , 2017, 54, 1777-1785.	4.0	12
94	The functional polymorphisms of LIS1 are associated with acute myeloid leukemia risk in a Han Chinese population. <i>Leukemia Research</i> , 2017, 54, 7-11.	0.8	5
95	Exome-Wide Association Study Identifies Low-Frequency Coding Variants in 2p23.2 and 7p11.2 Associated with Survival of Non-Small Cell Lung Cancer Patients. <i>Journal of Thoracic Oncology</i> , 2017, 12, 644-656.	1.1	10
96	Genetic variants, PM2.5 exposure level and global DNA methylation level: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2017, 269, 77-82.	0.8	10
97	Exome Array Analysis Identifies Variants in SPOCD1 and BTN3A2 That Affect Risk for Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, 2011-2021.	1.3	58
98	Potentially functional variants in lncRNAs are associated with breast cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 2048-2057.	2.7	11
99	A polymorphism in miR-1262 regulatory region confers the risk of lung cancer in Chinese population. <i>International Journal of Cancer</i> , 2017, 141, 958-966.	5.1	26
100	Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. <i>Gene</i> , 2017, 626, 414-419.	2.2	0
101	Genetically predicted high body mass index is associated with increased gastric cancer risk. <i>European Journal of Human Genetics</i> , 2017, 25, 1061-1066.	2.8	20
102	Targeted sequencing of chromosome 15q25 identified novel variants associated with risk of lung cancer and smoking behavior in Chinese. <i>Carcinogenesis</i> , 2017, 38, 552-558.	2.8	10
103	Genetic variants at 9p21.3 are associated with risk of esophageal squamous cell carcinoma in a Chinese population. <i>Cancer Science</i> , 2017, 108, 250-255.	3.9	14
104	Fine mapping of chromosome 5p15.33 identifies novel lung cancer susceptibility loci in Han Chinese. <i>International Journal of Cancer</i> , 2017, 141, 447-456.	5.1	17
105	Metabolome-wide association study identified the association between a circulating polyunsaturated fatty acids variant rs174548 and lung cancer. <i>Carcinogenesis</i> , 2017, 38, 1147-1154.	2.8	21
106	Fine-mapping the MHC region in Asian populations identified novel variants modifying susceptibility to lung cancer. <i>Lung Cancer</i> , 2017, 112, 169-175.	2.0	21
107	The sex ratio of singleton and twin delivery offspring in assisted reproductive technology in China. <i>Scientific Reports</i> , 2017, 7, 7754.	3.3	18
108	High mitochondrial DNA copy number was associated with an increased gastric cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 2593-2600.	2.7	32

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109	Genetic association of telomere length with hepatocellular carcinoma risk: A Mendelian randomization analysis. <i>Cancer Epidemiology</i> , 2017, 50, 39-45.	1.9	14
110	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. <i>Fertility and Sterility</i> , 2017, 108, 1056-1062.e4.	1.0	15
111	A cis-eQTL genetic variant of the cancer-associated testis gene CCDC116 is associated with risk of multiple cancers. <i>Human Genetics</i> , 2017, 136, 987-997.	3.8	7
112	Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. <i>Gene</i> , 2017, 627, 549-555.	2.2	21
113	Independent prognostic role of human papillomavirus genotype in cervical cancer. <i>BMC Infectious Diseases</i> , 2017, 17, 391.	2.9	43
114	Short leukocyte telomere length, alone and in combination with smoking, contributes to increased risk of gastric cancer or esophageal squamous cell carcinoma. <i>Carcinogenesis</i> , 2017, 38, 12-18.	2.8	14
115	Low-frequency nonsynonymous variants in <i>FKBP1</i> and <i>ARPC1B</i> genes are associated with breast cancer risk in Chinese women. <i>Molecular Carcinogenesis</i> , 2017, 56, 774-780.	2.7	12
116	Genetic variants affecting telomere length are associated with the prognosis of esophageal squamous cell carcinoma in a Chinese population. <i>Molecular Carcinogenesis</i> , 2017, 56, 1021-1029.	2.7	7
117	Estimation of heritability for nine common cancers using data from genome-wide association studies in Chinese population. <i>International Journal of Cancer</i> , 2017, 140, 329-336.	5.1	66
118	Genetic Variants in the Promoter Region of <i>miR-10b</i> and the Risk of Breast Cancer. <i>BioMed Research International</i> , 2017, 2017, 1-7.	1.9	7
119	Risk assessment models for genetic risk predictors of lung cancer using two-stage replication for Asian and European populations. <i>Oncotarget</i> , 2017, 8, 53959-53967.	1.8	11
120	Systematic identification of long non-coding RNAs with cancer-testis expression patterns in 14 cancer types. <i>Oncotarget</i> , 2017, 8, 94769-94779.	1.8	10
121	Functional polymorphisms in <i>NR3C1</i> are associated with gastric cancer risk in Chinese population. <i>Oncotarget</i> , 2017, 8, 105312-105319.	1.8	9
122	Family History and Stroke Risk in China: Evidence from a Large Cohort Study. <i>Journal of Stroke</i> , 2017, 19, 188-195.	3.2	21
123	Association of KCTD10, MVK, and MMAB polymorphisms with dyslipidemia and coronary heart disease in Han Chinese population. <i>Lipids in Health and Disease</i> , 2016, 15, 171.	3.0	18
124	Telomere length, genetic variants and risk of squamous cell carcinoma of the head and neck in Southeast Chinese. <i>Scientific Reports</i> , 2016, 6, 20675.	3.3	13
125	The known genetic loci for telomere length may be involved in the modification of telomeres length after birth. <i>Scientific Reports</i> , 2016, 6, 38729.	3.3	17
126	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	2.9	50

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127	The association between telomere length and cancer risk in population studies. Scientific Reports, 2016, 6, 22243.	3.3	101
128	Genetic variants in chromatin-remodeling pathway associated with lung cancer risk in a Chinese population. Gene, 2016, 587, 178-182.	2.2	9
129	Role of <i>ATG10</i> expression quantitative trait loci in non-small cell lung cancer survival. International Journal of Cancer, 2016, 139, 1564-1573.	5.1	55
130	Systematic identification of genes with a cancer-testis expression pattern in 19 cancer types. Nature Communications, 2016, 7, 10499.	12.8	124
131	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	2.9	50
132	Commentary: Post-GWAS era: What can we do beyond cancer genetic association studies?. International Journal of Epidemiology, 2016, 45, 221-222.	1.9	1
133	Genetic variants in multisynthetase complex genes are associated with DNA damage levels in Chinese populations. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2016, 786, 8-13.	1.0	6
134	Fine mapping the MHC region identified four independent variants modifying susceptibility to chronic hepatitis B in Han Chinese. Human Molecular Genetics, 2016, 25, 1225-1232.	2.9	33
135	Genetic variants in regulatory regions of microRNAs are associated with lung cancer risk. Oncotarget, 2016, 7, 47966-47974.	1.8	28
136	miR-486-5p expression pattern in esophageal squamous cell carcinoma, gastric cancer and its prognostic value. Oncotarget, 2016, 7, 15840-15853.	1.8	28
137	Potentially functional polymorphisms in PAK 1 are associated with risk of lung cancer in a Chinese population. Cancer Medicine, 2015, 4, 1781-1787.	2.8	6
138	The eQTL-missense polymorphisms of APOBEC3H are associated with lung cancer risk in a Han Chinese population. Scientific Reports, 2015, 5, 14969.	3.3	15
139	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152
140	Cumulative Effect and Predictive Value of Genetic Variants Associated with Type 2 Diabetes in Han Chinese: A Case-Control Study. PLoS ONE, 2015, 10, e0116537.	2.5	19
141	Potentially Functional Polymorphisms in <i>POU5F1</i> Gene Are Associated with the Risk of Lung Cancer in Han Chinese. BioMed Research International, 2015, 2015, 1-7.	1.9	3
142	Systematical analyses of variants in CTCF-binding sites identified a novel lung cancer susceptibility locus among Chinese population. Scientific Reports, 2015, 5, 7833.	3.3	16
143	Genetic variants of H2AX gene were associated with P M 2.5 -modulated DNA damage levels in Chinese Han populations. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 778, 41-45.	1.0	3
144	Joint effect of CENTD2 and KCNQ1 polymorphisms on the risk of type 2 diabetes mellitus among Chinese Han population. Molecular and Cellular Endocrinology, 2015, 407, 46-51.	3.2	12

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145	Personal exposure to PM2.5, genetic variants and DNA damage: A multi-center population-based study in Chinese. <i>Toxicology Letters</i> , 2015, 235, 172-178.	0.8	34
146	Plasma miRNA as early biomarkers for detecting hepatocellular carcinoma. <i>International Journal of Cancer</i> , 2015, 137, 1679-1690.	5.1	188
147	Low-Frequency Coding Variants at 6p21.33 and 20q11.21 Are Associated with Lung Cancer Risk in Chinese Populations. <i>American Journal of Human Genetics</i> , 2015, 96, 832-840.	6.2	41
148	Association analysis identifies new risk loci for congenital heart disease in Chinese populations. <i>Nature Communications</i> , 2015, 6, 8082.	12.8	26
149	Polymorphisms in alternative splicing associated genes are associated with lung cancer risk in a Chinese population. <i>Lung Cancer</i> , 2015, 89, 238-242.	2.0	9
150	Telomere length, genetic variants and gastric cancer risk in a Chinese population. <i>Carcinogenesis</i> , 2015, 36, 963-970.	2.8	46
151	U-shaped association between telomere length and esophageal squamous cell carcinoma risk: a case-control study in Chinese population. <i>Frontiers of Medicine</i> , 2015, 9, 478-486.	3.4	10
152	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015, 24, 1791-1800.	2.9	105
153	Potentially functional polymorphisms in aminoacyl-tRNA synthetases genes are associated with breast cancer risk in a Chinese population. <i>Molecular Carcinogenesis</i> , 2015, 54, 577-583.	2.7	15
154	Pathway analysis for a genome-wide association study of pneumoconiosis. <i>Toxicology Letters</i> , 2015, 232, 284-292.	0.8	8
155	Circulating Tumor Cells Enriched by the Depletion of Leukocytes with Bi-Antibodies in Non-Small Cell Lung Cancer: Potential Clinical Application. <i>PLoS ONE</i> , 2015, 10, e0137076.	2.5	18
156	Genetic Variation in the 3'-Untranslated Region of NBN Gene Is Associated with Gastric Cancer Risk in a Chinese Population. <i>PLoS ONE</i> , 2015, 10, e0139059.	2.5	7
157	A functional variant in miR-155 regulation region contributes to lung cancer risk and survival. <i>Oncotarget</i> , 2015, 6, 42781-42792.	1.8	47
158	Genetic Variations in the Flanking Regions of miR-101-2 Are Associated with Increased Risk of Breast Cancer. <i>PLoS ONE</i> , 2014, 9, e86319.	2.5	19
159	Genetic Variants at 10p11 Confer Risk of Tetralogy of Fallot in Chinese of Nanjing. <i>PLoS ONE</i> , 2014, 9, e89636.	2.5	6
160	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	21.4	148
161	A genome-wide gene-environment interaction analysis for tobacco smoke and lung cancer susceptibility. <i>Carcinogenesis</i> , 2014, 35, 1528-1535.	2.8	47
162	Genetic variants in SMAR genes are associated with DNA damage levels in Chinese population. <i>Toxicology Letters</i> , 2014, 229, 327-332.	0.8	6

#	ARTICLE	IF	CITATIONS
163	Association analysis identifies new risk loci for non-obstructive azoospermia in Chinese men. Nature Communications, 2014, 5, 3857.	12.8	64
164	Genetic variants at 10q23.33 are associated with plasma lipid levels in a Chinese population. Journal of Biomedical Research, 2014, 28, 53-8.	1.6	5
165	Genetic variants at 4q21, 4q23 and 12q24 are associated with esophageal squamous cell carcinoma risk in a Chinese population. Human Genetics, 2013, 132, 649-656.	3.8	34
166	New loci associated with chronic hepatitis B virus infection in Han Chinese. Nature Genetics, 2013, 45, 1499-1503.	21.4	140
167	Human genome epidemiology, progress and future. Journal of Biomedical Research, 2013, 27, 167-169.	1.6	17
168	Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. Nature Genetics, 2012, 44, 895-899.	21.4	129
169	Genetic Variants at 6p21.1 and 7p15.3 Are Associated with Risk of Multiple Cancers in Han Chinese. American Journal of Human Genetics, 2012, 91, 928-934.	6.2	76
170	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	21.4	238
171	A genome-wide association study identifies two new lung cancer susceptibility loci at 13q12.12 and 22q12.2 in Han Chinese. Nature Genetics, 2011, 43, 792-796.	21.4	340
172	Genome-wide association study identifies three new susceptibility loci for esophageal squamous-cell carcinoma in Chinese populations. Nature Genetics, 2011, 43, 679-684.	21.4	260
173	A genome-wide association study identifies new susceptibility loci for non-cardia gastric cancer at 3q13.31 and 5p13.1. Nature Genetics, 2011, 43, 1215-1218.	21.4	250
174	Genetic variants at 1q22 and 10q23 reproducibly associated with gastric cancer susceptibility in a Chinese population. Carcinogenesis, 2011, 32, 848-852.	2.8	73
175	Genetic variants in one-carbon metabolism-related genes contribute to NSCLC prognosis in a Chinese population. Cancer, 2010, 116, 5700-5709.	4.1	14
176	The 5p15.33 Locus Is Associated with Risk of Lung Adenocarcinoma in Never-Smoking Females in Asia. PLoS Genetics, 2010, 6, e1001051.	3.5	168
177	Common genetic variants on 5p15.33 contribute to risk of lung adenocarcinoma in a Chinese population. Carcinogenesis, 2009, 30, 987-990.	2.8	72
178	Putative functional polymorphisms of <i>MMP9</i> predict survival of NSCLC in a Chinese population. International Journal of Cancer, 2009, 124, 2172-2178.	5.1	22